

SEQUENCE LISTING

<110> OXAGEN LIMITED

<120> Ligand

<130> N.89652C GCW

<150> GB 0328275.3

<151> 2003-12-05

<150> GB 0403014.4

<151> 2004-02-11

<150> GB 0418568.2

<151> 2004-08-19

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<170> PatentIn version 3.2

<210> 1

<211> 1531

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (48) .. (1118)

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Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr Thr Leu Ala
5 10 15

cca gag gat gaa tat gat gtc ctc ata gaa ggt gaa ctg gag agc gat 152
Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu Glu Ser Asp
20 25 30 35

gag gca gag caa tgt gac aag tat gac gcc cag gca ctc tca gcc cag 200
Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu Ser Ala Gln
40 45 50

ctg gtg cca tca ctc tgc tct gct gtg ttt gtg atc ggt gtc ctg gac 248
Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly Val Leu Asp
55 60 65

aat ctc ctg gtt gtg ctt atc ctg gta aaa tat aaa gga ctc aaa cgc 296
Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly Leu Lys Arg
70 75 80

gtg gaa aat atc tat ctt cta aac ttg gca gtt tct aac ttg tgt ttc 344
Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn Leu Cys Phe
85 90 95

ttg ctt acc ctg ccc ttc tgg gct cat gct ggg ggc gat ccc atg tgt	392
Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp Pro Met Cys	
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aaa att ctc att gga ctg tac ttc gtg ggc ctg tac agt gag aca ttt	440
Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser Glu Thr Phe	
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Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe Leu His Lys	
135 140 145	
ggc aac ttt ttc tca gcc agg agg agg gtg ccc tgt ggc atc att aca	536
Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly Ile Ile Thr	
150 155 160	
agt gtc ctg gca tgg gta aca gcc att ctg gcc act ttg cct gaa tac	584
Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu Pro Glu Tyr	
165 170 175	
gtg gtt tat aaa cct cag atg gaa gac cag aaa tac aag tgt gca ttt	632
Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys Cys Ala Phe	
180 185 190 195	
agc aga act ccc ttc ctg cca gct gat gag aca ttc tgg aag cat ttt	680
Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp Lys His Phe	
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Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro Leu Phe Ile	
215 220 225	
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Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg Phe Arg Glu	
230 235 240	
cag agg tat agc ctt ttc aag ctt gtt ttt gcc ata atg gta gtc ttc	824
Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Ile Met Val Val Phe	
245 250 255	
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Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu Ser Thr Phe	
260 265 270 275	
aaa gaa cac ttc tcc ctg agt gac tgc aag agc agc tac aat ctg gac	920
Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr Asn Leu Asp	
280 285 290	
aaa agt gtt cac atc act aaa ctc atc gcc acc acc cac tgc tgc atc	968
Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His Cys Cys Ile	
295 300 305	
aac cct ctc ctg tat gcg ttt ctt gat ggg aca ttt agc aaa tac ctc	1016
Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser Lys Tyr Leu	
310 315 320	
tgc cgc tgt ttc cat ctg cgt agt aac acc cca ctt caa ccc agg ggg	1064
Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln Pro Arg Gly	
325 330 335	

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 Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His Ser Thr Glu
 340 345 350 355

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 Val

gcattatttc atgtaaattt tctacacatt tgtatacaaa atcggataca ggaagaaaag 1228

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aaa 1531

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<212> PRT

<213> Homo sapiens

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 35 40 45

Ser Ala Gln Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly
 50 55 60

Val Leu Asp Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly
 65 70 75 80

Leu Lys Arg Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn
 85 90 95

Leu Cys Phe Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp
 100 105 110

Pro Met Cys Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser
 115 120 125

Glu Thr Phe Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe
 130 135 140

Leu His Lys Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly

145		150		155		160
Ile Ile Thr Ser Val	Leu Ala Trp Val	Thr Ala Ile Leu Ala	Thr Leu			
	165	170	175			
Pro Glu Tyr Val Val	Tyr Lys Pro Gln Met Glu Asp Gln	Lys Tyr Lys				
	180	185	190			
Cys Ala Phe Ser Arg Thr	Pro Phe Leu Pro Ala Asp Glu Thr	Phe Trp				
	195	200	205			
Lys His Phe Leu Thr	Leu Lys Met Asn Ile Ser Val	Leu Val Leu Pro				
	210	215	220			
Leu Phe Ile Phe Thr	Phe Leu Tyr Val Gln Met Arg Lys Thr	Leu Arg				
	225	230	235			240
Phe Arg Glu Gln Arg	Tyr Ser Leu Phe Lys Leu Val Phe Ala	Ile Met				
	245	250	255			
Val Val Phe Leu Leu Met	Trp Ala Pro Tyr Asn Ile Ala Phe Phe	Leu				
	260	265	270			
Ser Thr Phe Lys Glu His	Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr					
	275	280	285			
Asn Leu Asp Lys Ser Val	His Ile Thr Lys Leu Ile Ala Thr Thr	His				
	290	295	300			
Cys Cys Ile Asn Pro Leu Leu Tyr	Ala Phe Leu Asp Gly Thr Phe Ser					
	305	310	315			320
Lys Tyr Leu Cys Arg Cys Phe His	Leu Arg Ser Asn Thr Pro Leu Gln					
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atttcagttg gtcctgagc tcggtgagtg gggcgggtag agccaccagg ggaatcaaca	180

gtggtttctc	gtgccccctca	gggtcaggag	cagtctgatac	aaaaggaggg	catccactgt	240
ccggggccat	tcccacagct	cccggatgct	gggtctggag	gctgcgccct	tcccctgcag	300
gagctcagcc	cagtgggcag	tctgaag	atg gcc aat tac acg ctg gca cca gag	354		
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gat gaa tat gat gtc ctc ata gaa ggt gaa ctg gag agc gat gag gca	402					
Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu Glu Ser Asp Glu Ala						
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Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu Ser Ala Gln Leu Val						
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cca tca ctc tgc tct gct gtg ttt gtg atc ggt gtc ctg gac aat ctc	498					
Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly Val Leu Asp Asn Leu						
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ctg gtt gtg ctt atc ctg gta aaa tat aaa gga ctc aaa cgc gtg gaa	546					
Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly Leu Lys Arg Val Glu						
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Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn Leu Cys Phe Leu Leu						
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acc ctg ccc ttc tgg gct cat gct ggg ggc gat ccc atg tgt aaa att	642					
Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp Pro Met Cys Lys Ile						
90 95 100 105						
ctc att gga ctg tac ttc gtg ggc ctg tac agt gag aca ttt ttc aat	690					
Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser Glu Thr Phe Phe Asn						
110 115 120						
tgc ctt ctg act gtg caa agg tac cta gtg ttt ttg cac aag ggc aac	738					
Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe Leu His Lys Gly Asn						
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Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly Ile Ile Thr Ser Val						
140 145 150						
ctg gca tgg gta aca gcc att ctg gcc act ttg cct gaa tac gtg gtt	834					
Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu Pro Glu Tyr Val Val						
155 160 165						
tat aaa cct cag atg gaa gac cag aaa tac aag tgt gca ttt agc aga	882					
Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys Cys Ala Phe Ser Arg						
170 175 180 185						
act ccc ttc ctg cca gct gat gag aca ttc tgg aag cat ttt ctg act	930					
Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp Lys His Phe Leu Thr						
190 195 200						
tta aaa atg aac att tcg gtt ctt gtc ctc ccc cta ttt att ttt aca	978					
Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro Leu Phe Ile Phe Thr						
205 210 215						

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 Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg Phe Arg Glu Gln Arg
 220 225 230

tat agc ctt ttc aag ctt gtt ttt gcc ata atg gta gtc ttc ctt ctg 1074
 Tyr Ser Leu Phe Lys Leu Val Phe Ala Ile Met Val Val Phe Leu Leu
 235 240 245

atg tgg gcg ccc tac aat att gca ttt ttc ctg tcc act ttc aaa gaa 1122
 Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu Ser Thr Phe Lys Glu
 250 255 260 265

cac ttc tcc ctg agt gac tgc aag agc agc tac aat ctg gac aaa agt 1170
 His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr Asn Leu Asp Lys Ser
 270 275 280

gtt cac atc act aaa ctc atc gcc acc acc cac tgc tgc atc aac cct 1218
 Val His Ile Thr Lys Leu Ile Ala Thr Thr His Cys Cys Ile Asn Pro
 285 290 295

ctc ctg tat gcg ttt ctt gat ggg aca ttt agc aaa tac ctc tgc cgc 1266
 Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser Lys Tyr Leu Cys Arg
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 Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln Pro Arg Gly Gln Ser
 315 320 325

gca caa ggc aca tcg agg gaa gaa cct gac cat tcc acc gaa gtg taa 1362
 Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His Ser Thr Glu Val
 330 335 340

actagcatcc accaaatgca agaagaataa acatggattt tcatcttttct gcattatttc 1422

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gctaacattt gctaagcact gaatttgtct caggcaccgt gcaaggctct ttacaaacgt 1542

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agaagaaaac taaggcgcgg aaatttgtct aagatcacat aactaggaag tggcagaact 1662

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<212> PRT

<213> Homo sapiens

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Phe	Val	Ile	Gly	Val	Leu	Asp	Asn	Leu	Leu	Val	Val	Leu	Ile	Leu	Val
	50					55					60				
Lys	Tyr	Lys	Gly	Leu	Lys	Arg	Val	Glu	Asn	Ile	Tyr	Leu	Leu	Asn	Leu
	65					70					75				80
Ala	Val	Ser	Asn	Leu	Cys	Phe	Leu	Leu	Thr	Leu	Pro	Phe	Trp	Ala	His
				85					90					95	
Ala	Gly	Gly	Asp	Pro	Met	Cys	Lys	Ile	Leu	Ile	Gly	Leu	Tyr	Phe	Val
			100					105					110		
Gly	Leu	Tyr	Ser	Glu	Thr	Phe	Phe	Asn	Cys	Leu	Leu	Thr	Val	Gln	Arg
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Tyr	Leu	Val	Phe	Leu	His	Lys	Gly	Asn	Phe	Phe	Ser	Ala	Arg	Arg	Arg
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Val	Pro	Cys	Gly	Ile	Ile	Thr	Ser	Val	Leu	Ala	Trp	Val	Thr	Ala	Ile
	145					150					155				160
Leu	Ala	Thr	Leu	Pro	Glu	Tyr	Val	Val	Tyr	Lys	Pro	Gln	Met	Glu	Asp
				165					170					175	
Gln	Lys	Tyr	Lys	Cys	Ala	Phe	Ser	Arg	Thr	Pro	Phe	Leu	Pro	Ala	Asp
			180					185					190		
Glu	Thr	Phe	Trp	Lys	His	Phe	Leu	Thr	Leu	Lys	Met	Asn	Ile	Ser	Val
		195					200					205			
Leu	Val	Leu	Pro	Leu	Phe	Ile	Phe	Thr	Phe	Leu	Tyr	Val	Gln	Met	Arg
	210					215					220				
Lys	Thr	Leu	Arg	Phe	Arg	Glu	Gln	Arg	Tyr	Ser	Leu	Phe	Lys	Leu	Val
	225					230					235				240
Phe	Ala	Ile	Met	Val	Val	Phe	Leu	Leu	Met	Trp	Ala	Pro	Tyr	Asn	Ile
				245					250					255	
Ala	Phe	Phe	Leu	Ser	Thr	Phe	Lys	Glu	His	Phe	Ser	Leu	Ser	Asp	Cys
			260					265					270		
Lys	Ser	Ser	Tyr	Asn	Leu	Asp	Lys	Ser	Val	His	Ile	Thr	Lys	Leu	Ile
		275					280					285			
Ala	Thr	Thr	His	Cys	Cys	Ile	Asn	Pro	Leu	Leu	Tyr	Ala	Phe	Leu	Asp
	290					295					300				
Gly	Thr	Phe	Ser	Lys	Tyr	Leu	Cys	Arg	Cys	Phe	His	Leu	Arg	Ser	Asn
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Thr	Pro	Leu	Gln	Pro	Arg	Gly	Gln	Ser	Ala	Gln	Gly	Thr	Ser	Arg	Glu
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1 5 10 15
ctc tgc tcc tgt gca caa gtt ggt acc aac aaa gag ctc tgc tgc ctc 156
Leu Cys Ser Cys Ala Gln Val Gly Thr Asn Lys Glu Leu Cys Cys Leu
20 25 30
gtc tat acc tcc tgg cag att cca caa aag ttc ata gtt gac tat tct 204
Val Tyr Thr Ser Trp Gln Ile Pro Gln Lys Phe Ile Val Asp Tyr Ser
35 40 45
gaa acc agc ccc cag tgc ccc aag cca ggt gtc atc ctc cta acc aag 252
Glu Thr Ser Pro Gln Cys Pro Lys Pro Gly Val Ile Leu Leu Thr Lys
50 55 60
aga ggc cgg cag atc tgt gct gac ccc aat aag aag tgg gtc cag aaa 300
Arg Gly Arg Gln Ile Cys Ala Asp Pro Asn Lys Lys Trp Val Gln Lys
65 70 75 80
tac atc agc gac ctg aag ctg aat gcc tga ggggcctgga agctgcgagg 350
Tyr Ile Ser Asp Leu Lys Leu Asn Ala
85
gccagtgaa cttggtgggc ccaggaggga acaggagcct gagccagggc aatggccctg 410
ccaccctgga ggccacctct tctaagagtc ccattctgcta tgccagcca cattaactaa 470
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ttcccttcaa ctcttcgtac attcaatgca tggatcaatc agtgtgatta gctttctcag 650
cagacattgt gccatatgta tcaaatgaca aatctttatt gaatggtttt gctcagcacc 710
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<212> PRT

<213> Homo sapiens

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Val Tyr Thr Ser Trp Gln Ile Pro Gln Lys Phe Ile Val Asp Tyr Ser
35 40 45

Glu Thr Ser Pro Gln Cys Pro Lys Pro Gly Val Ile Leu Leu Thr Lys
50 55 60

Arg Gly Arg Gln Ile Cys Ala Asp Pro Asn Lys Lys Trp Val Gln Lys
65 70 75 80

Tyr Ile Ser Asp Leu Lys Leu Asn Ala
85